



SEQUENCE LISTING

<110> Ono Pharmaceutical Co., Ltd.

<120> A novel polypeptide, a cDNA encoding the polypeptide and utilization thereof

<130> Q61531

<140> 09/674,379

<141> 2000-10-30

<150> PCT/JP99/02284

<151> 1999-04-28

<150> JP 10-119731

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<170> PatentIn version 3.1

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Thr	Ser	Tyr	Ser	Gly	Pro	Tyr	Pro	Ala	Ala	Ala	Pro	Pro	Val	Pro	Ala			
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Arg	Leu	Arg	Ile	Tyr	Val	Ser	Gln	Tyr	Pro	Phe						
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gagcgagaca	gacattgcac	ctttcctgct	gaatatctcc	tgggggcatc	agcctagcat											1754

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<213> Mus musculus

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<223> Clone mouse A55b derived from Day 13 mouse embryonic heart

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Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val
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Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe
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Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys
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Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr
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Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu
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Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly
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Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys
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Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser
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Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile
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His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln
 225 230 235

His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro
 240 245 250

Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu

255

260

265

Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn
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Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro
 285 290 295 300

Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr
 305 310 315

Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val
 320 325 330

Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr
 335 340 345

Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn
 350 355 360

Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr
 365 370 375 380

Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp
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Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn
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Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser
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Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro
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Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu
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Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
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Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
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Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
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Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro
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Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp
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Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys
 180 185 190

Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
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Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp
 210 215 220

Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
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Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp
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Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys
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Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu
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Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro
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Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
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Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala
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Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr
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Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro
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Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val
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Met Pro Gly

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Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys Leu Pro Ser
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Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu
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Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser	
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Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu	
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Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn	
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Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala Glu Asn Pro	
305 310 315	
ggc tgc aga gac cag ccc ttt acc atc ttg tac cgg gac atg gac gtg	1233
Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val	

320	325	330	
gtg tca gga cgc tcc gtt ccc gct gac atc ttc caa atg caa gcc acg			1281
Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr			
335	340	345	
acc cgc tac cct ggg gcc tat tac att ttc cag atc aaa tct ggg aat			1329
Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn			
350	355	360	
gag ggc aga gaa ttt tac atg cgg caa acg ggc ccc atc agt gcc acc			1377
Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr			
365	370	375	380
ctg gtg atg aca cgc ccc atc aaa ggg ccc cgg gaa atc cag ctg gac			1425
Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp			
385	390	395	
ttg gaa atg atc act gtc aac act gtc atc aac ttc aga ggc agc tcc			1473
Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser			
400	405	410	
gtg atc cga ctg cgg ata tat gtg tcg cag tac cca ttc tgagcctcgg			1522
Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe			
415	420	425	
gctggagcct ccgacgctgc ctctcattgg caccaaggga caggagaaga gaggaaataa			1582
cagagagaat gagagcgaca cagacgttag gcatttcctg ctgaacgttt ccccgaagag			1642
tcagccccga cttcctgact ctcacctgta ctattgcaga cctgtcacc tgcaggactt			1702
gccacccccca gttcctatga tacagttatc aaaaagtatt atcattgctc ccctgataga			1762
agattgttgg tgaattttca aggccttcag tttattttcca ctattttcaa agaaaataga			1822
ttaggtttgc gggggtctga gtctatgttc aaagactgtg aacagcttgc tgtcacttct			1882
tcacctcttc cactccttct ctactgtgt tactgctttg caaagaccg ggagctggcg			1942
gggaaccctg ggagtagcta gtttgctttt tgcgtacaca gagaaggcta tgtaaacaaa			2002
ccacagcagg atcgaagggt ttttagagaa tgtgtttcaa aaccatgcct ggtattttca			2062
accataaaaag aagtttcagt tgtccttaaa tttgtataac ggtttaattc tgtcttgttc			2122
attttgagta tttttaaaaa atatgtcgta gaattccttc gaaaggcctt cagacacatg			2182
ctatgttctg tcttcccaa cccagtctcc tctccatttt agcccagtgt tttctttgag			2242
gaccccttaa tcttgctttc tttagaattt ttacccaatt ggattggaat gcagaggtct			2302
ccaaactgat taaatatttg aagaga			2328

<210> 13
<211> 448
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Clone human A55 derived from human brain

<400> 13

Met Pro Gly Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys
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Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp
-5 -1 1 5

Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
10 15 20 25

Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
30 35 40

Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
45 50 55

Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
60 65 70

Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile
75 80 85

Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val
90 95 100 105

Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
110 115 120

Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
125 130 135

Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
140 145 150

Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
 155 160 165

Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val
 170 175 180 185

Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
 190 195 200

Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
 205 210 215

Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
 220 225 230

Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser
 235 240 245

Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
 250 255 260 265

Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr
 270 275 280

Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys
 285 290 295

Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala
 300 305 310

Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
 315 320 325

Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
 330 335 340 345

Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
 350 355 360

Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
 365 370 375

Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile
380 385 390

Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
395 400 405

Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
410 415 420 425

<210> 14
<211> 423
<212> PRT
<213> Homo sapiens

<400> 14

Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu
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Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met
20 25 30

Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn
35 40 45

Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro Tyr Ser
50 55 60

Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn Tyr Pro
65 70 75 80

Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe Gly Tyr Gln Met Asp Glu
85 90 95

Ser Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
100 105 110

Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
115 120 125

Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
130 135 140

Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro
145 150 155 160

Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Glu Asp
165 170 175

Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Ala Thr Glu Asn Pro Cys
180 185 190

Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
195 200 205

Pro Gly Tyr Glu Leu Glu Glu Asp Gly Val His Cys Ser Asp Met Asp
210 215 220

Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
225 230 235 240

Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Ile Leu Leu Asp
245 250 255

Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His
260 265 270

Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys
275 280 285

Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile Ser Asp
290 295 300

Asn Arg Cys Met Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp Gln Pro
305 310 315 320

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
325 330 335

Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala
340 345 350

Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr
355 360 365

Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro
 370 375 380

Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu Glu Met Ile Thr Val
 385 390 395 400

Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile
 405 410 415

Tyr Val Ser Gln Tyr Pro Phe
 420

<210> 15
 <211> 1269
 <212> DNA
 <213> Homo sapiens

<400> 15
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 tattttatgca ttccccggac aaaccctgtg tatcgagggc cctactcgaa cccctactcg 180
 accccctact caggctcgta cccagcagct gccccaccac tctcagctcc aaactatccc 240
 acgatctcca ggctctttat atgccgcttt ggataccaga tggatgaaag caaccaatgt 300
 gtggatgtgg acgagtgtgc aacagattcc caccagtgc accccacca gatctgcatc 360
 aatactgaag gcgggtacac ctgctcctgc accgacggat attggcttct ggaaggccag 420
 tgcttagaca ttgatgaatg tcgctatggt tactgccagc agctctgtgc gaatgttcct 480
 ggatcctatt cttgtacatg caaccctggg tttaccctca atgaggatgg aaggctctgc 540
 caagatgtga acgagtgtgc caccgagaac cctgcgtgc aaacctgcgt caacacctac 600
 ggctctttca tctgccgctg tgaccagga tatgaacttg aggaagatgg cgttcattgc 660
 agtgatatgg acgagtgcag cttctctgag ttctctgcc aacatgagtg tgtgaaccag 720
 cccggcacat acttctgctc ctgccctcca ggctacatcc tgctggatga caaccgaagc 780
 tgccaagaca tcaacgaatg tgagcacagg aaccacacgt gcaacctgca gcagacgtgc 840
 tacaatttac aaggggggctt caaatgcatc gaccccatcc gctgtgagga gccttatctg 900
 aggatcagtg ataaccgctg tatgtgtcct gctgagaacc ctggctgcag agaccagccc 960

tttaccatct tgtaccggga catggacgtg gtgtcaggac gctccgttcc cgctgacatc 1020
 ttccaaatgc aagccacgac ccgctaccct ggggcctatt acattttcca gatcaaactc 1080
 ggggaatgagg gcagagaatt ttacatgcgg caaacggggc ccatcagtgc caccctggtg 1140
 atgacacgcc ccatcaaagg gccccgggaa atccagctgg acttggaat gatcactgtc 1200
 aacactgtca tcaacttcag aggcagctcc gtgatccgac tgcggatata tgtgtcgcag 1260
 taccattc 1269

<210> 16
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> misc_feature
 <222> (27)..(35)
 <223> "n" may be a, c, g or t

<400> 16 35
 cgattgaatt ctagacctgc ctgagnnnn nnnnn

<210> 17
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 17 27
 cgtttgtgca ctgctgctgt gcattcc